

## SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> A novel polypeptide, a cDNA encoding the polypeptide  
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<150> PCT/JP99/02284

<151> 1999-04-28

<150> JP HEI 10-119731

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<170> PatentIn Ver. 2.1

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Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser  
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aca tcc tac tca ggc cca tac cca gca gcg gcc cca cca gta cca gct 573  
Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala  
65 70 75

tcc aac tac ccc acg att tca agg cct ctt gtc tgc cgc ttt ggg tat 621  
Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr  
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cag atg gat gaa ggc aac cag tgt gtg gat gtg gac gag tgt gca aca	669
Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr	
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Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly	
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Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln	
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Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys	
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 gca aat gtt cca gga tcc tat tcc tgt aca tgc aac cct ggt ttc acc	861
Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr	
160 165 170	
 ctc aac gac gat gga agg tct tgc caa gat gtg aac gag tgc gaa act	909
Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr	
175 180 185 190	
 gag aat ccc tgt gtt cag acc tgt gtc aac acc tat ggc tct ttc atc	957
Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile	
195 200 205	
 tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc att cac tgc	1005
Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys	
210 215 220	
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Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu	
225 230 235	
 tgt gtg aac cag ccg ggc tca tac ttc tgc tcg tgc cct cca ggc tac	1101
Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr	
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Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu	
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 cac cga aac cac acg tgt acc tca ctg cag act tgc tac aat cta caa	1197
His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln	
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 Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu  
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ctg att ggt gaa aac cgc tgt atg tgt cct gct gag cac acc agc tgc 1293  
 Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys  
 305 310 315

aga gac cag cca ttc acc atc ctg tat cgg gac atg gat gtg gtg tca 1341  
 Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser  
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gga cgc tcc gtt cct gct gac atc ttc cag atg caa gca aca acc cga 1389  
 Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg  
 335 340 345 350

tac cct ggt gcc tat tac att ttc cag atc aaa tct ggc aac gag ggt 1437  
 Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly  
 355 360 365

cga gag ttc tat atg cgg caa aca ggg cct atc agt gcc acc ctg gtg 1485  
 Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val  
 370 375 380

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 Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu  
 385 390 395

atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc gtg atc 1581  
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cga ctg cgg ata tat gtg tcg cag tat ccg ttc tgagcctctg gctaaggcct 1634  
 Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe  
 415 420 425

ctgacactgc ctttcaccag caccgagggg cgggaggaga aaggaaacca gcaagaatga 1694

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 <212> PRT  
 <213> Mus musculus  
 <223> Clone mouse A55b derived from Day 13 mouse  
 embryonic heart

<400> 8  
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 Pro Gly Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg  
 -1 1 5 10  
 Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu  
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 Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu  
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 Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro  
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 Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val  
 65 70 75  
 Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe  
 80 85 90

Gly	Tyr	Gln	Met	Asp	Glu	Gly	Asn	Gln	Cys	Val	Asp	Val	Asp	Glu	Cys	95	100	105	
Ala	Thr	Asp	Ser	His	Gln	Cys	Asn	Pro	Thr	Gln	Ile	Cys	Ile	Asn	Thr	110	115	120	
Glu	Gly	Gly	Tyr	Thr	Cys	Ser	Cys	Thr	Asp	Gly	Tyr	Trp	Leu	Leu	Glu	125	130	135	140
Gly	Gln	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Gly	Tyr	Cys	Gln	Gln	145	150	155	
Leu	Cys	Ala	Asn	Val	Pro	Gly	Ser	Tyr	Ser	Cys	Thr	Cys	Asn	Pro	Gly	160	165	170	
Phe	Thr	Leu	Asn	Asp	Asp	Gly	Arg	Ser	Cys	Gln	Asp	Val	Asn	Glu	Cys	175	180	185	
Glu	Thr	Glu	Asn	Pro	Cys	Val	Gln	Thr	Cys	Val	Asn	Thr	Tyr	Gly	Ser	190	195	200	
Phe	Ile	Cys	Arg	Cys	Asp	Pro	Gly	Tyr	Glu	Leu	Glu	Glu	Asp	Gly	Ile	205	210	215	220
His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	Phe	Ser	Glu	Phe	Leu	Cys	Gln	225	230	235	
His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Ser	Tyr	Phe	Cys	Ser	Cys	Pro	Pro	240	245	250	
Gly	Tyr	Val	Leu	Leu	Asp	Asp	Asn	Arg	Ser	Cys	Gln	Asp	Ile	Asn	Glu	255	260	265	
Cys	Glu	His	Arg	Asn	His	Thr	Cys	Thr	Ser	Leu	Gln	Thr	Cys	Tyr	Asn	270	275	280	
Leu	Gln	Gly	Gly	Phe	Lys	Cys	Ile	Asp	Pro	Ile	Ser	Cys	Glu	Glu	Pro	285	290	295	300
Tyr	Leu	Leu	Ile	Gly	Glu	Asn	Arg	Cys	Met	Cys	Pro	Ala	Glu	His	Thr	305	310	315	
Ser	Cys	Arg	Asp	Gln	Pro	Phe	Thr	Ile	Leu	Tyr	Arg	Asp	Met	Asp	Val	320	325	330	
Val	Ser	Gly	Arg	Ser	Val	Pro	Ala	Asp	Ile	Phe	Gln	Met	Gln	Ala	Thr	335	340	345	

Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn  
 350 355 360

Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr  
 365 370 375 380

Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp  
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Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser  
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Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe  
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 35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser  
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Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro  
 65 70 75 80

Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu  
 85 90 95

Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln  
 100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys  
 115 120 125



Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile  
 130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro  
 145 150 155 160

Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp  
 165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys  
 180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp  
 195 200 205

Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp  
 210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln  
 225 230 235 240

Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp  
 245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His  
 260 265 270

Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys  
 275 280 285

Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu  
 290 295 300

Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro  
 305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val  
 325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala  
 340 345 350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr  
 355 360 365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro  
 370 375 380

Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val  
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Tyr Val Ser Gln Tyr Pro Phe  
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<220>

<223> Clone human A55 derived from human brain

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<221> CDS

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<220>

<221> sig\_peptide

<222> (169)..(237)

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<222> (238)..(1512)

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cgcgagcttt cttctcgct tcgcatctcc tcctcgcgcg tcttggac atg cca gga 177  
 Met Pro Gly

ata aaa agg ata ctc act gtt acc att ctg gct ctc tgt ctt cca agc 225  
 Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys Leu Pro Ser  
 -20 -15 -10 -5

cct ggg aat gca cag gca cag tgc acg aat ggc ttt gac ctg gat cgc 273  
 Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg  
 -1 1 5 10

cag tca gga cag tgt tta gat att gat gaa tgc cga acc atc ccc gag 321  
 Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu  
 15 20 25

gcc tgc cga gga gac atg atg tgt gtt aac caa aat ggc ggg tat tta 369  
 Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu  
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tgc att ccc cgg aca aac cct gtg tat cga ggg ccc tac tcg aac ccc 417  
 Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro  
 45 50 55 60

tac tcg acc ccc tac tca ggt ccg tac cca gca gct gcc cca cca ctc 465  
 Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu  
 65 70 75

tca gct cca aac tat ccc acg atc tcc agg cct ctt ata tgc cgc ttt 513  
 Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe  
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gga tac cag atg gat gaa agc aac caa tgt gtg gat gtg gac gag tgt 561  
 Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys  
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gca aca gat tcc cac cag tgc aac ccc acc cag atc tgc atc aat act 609  
 Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr  
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gaa ggc ggg tac acc tgc tcc tgc acc gac gga tat tgg ctt ctg gaa 657  
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 Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln  
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ctc tgt gcg aat gtt cct gga tcc tat tct tgt aca tgc aac cct ggt 753

Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly  
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 175 180 185

gcc acc gag aac ccc tgc gtg caa acc tgc gtc aac acc tac ggc tct 849  
 Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser  
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ttc atc tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc gtt 897  
 Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val  
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cat tgc agt gat atg gac gag tgc agc ttc tct gag ttc ctc tgc caa 945  
 His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln  
 225 230 235

cat gag tgt gtg aac cag ccc ggc aca tac ttc tgc tcc tgc cct cca 993  
 His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro  
 240 245 250

ggc tac atc ctg ctg gat gac aac cga agc tgc caa gac atc aac gaa 1041  
 Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu  
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tgt gag cac agg aac cac acg tgc aac ctg cag cag acg tgc tac aat 1089  
 Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn  
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ggc tgc aga gac cag ccc ttt acc atc ttg tac cgg gac atg gac gtg 1233  
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Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn	
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Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp	
385 390 395	
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Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe	
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 <223> Clone human A55 derived from human brain

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Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr  
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Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly  
 30 35 40

Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr  
 45 50 55

Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala  
 60 65 70

Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile  
 75 80 85

Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val  
 90 95 100 105

Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys  
 110 115 120

Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp  
 125 130 135

Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr  
 140 145 150

Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys  
 155 160 165

Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val  
 170 175 180 185

Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr  
 190 195 200

Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu  
 205 210 215  
 Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe  
 220 225 230  
 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser  
 235 240 245  
 Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp  
 250 255 260 265  
 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr  
 270 275 280  
 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys  
 285 290 295  
 Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala  
 300 305 310  
 Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp  
 315 320 325  
 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met  
 330 335 340 345  
 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys  
 350 355 360  
 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile  
 365 370 375  
 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile  
 380 385 390  
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 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe  
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<210> 14  
 <211> 423  
 <212> PRT



<213> Homo sapiens

<400> 14

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35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser  
50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro  
65 70 75 80

Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp Glu  
85 90 95

Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln  
100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys  
115 120 125

Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile  
130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro  
145 150 155 160

Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Glu Asp  
165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn Pro Cys  
180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp  
195 200 205

Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val His Cys Ser Asp Met Asp  
210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln  
225 230 235 240

Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp  
 245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His  
 260 265 270

Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys  
 275 280 285

Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp  
 290 295 300

Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro  
 305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val  
 325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala  
 340 345 350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr  
 355 360 365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro  
 370 375 380

Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val  
 385 390 395 400

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Tyr Val Ser Gln Tyr Pro Phe  
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<210> 15

<211> 1269

<212> DNA

<213> Homo sapiens

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 tatttatgca ttccccggac aaaccctgtg tatcgagggc cctactcgaa cccctactcg 180  
 accccctact caggtccgta cccagcagct gccccaccac tctcagctcc aaactatccc 240  
 acgatctcca ggcctcttat atgccgcttt ggataccaga tggatgaaag caaccaatgt 300

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gtggatgtgg acgagtgtgc aacagattcc caccagtgc accccaccca gatctgcatc 360
aataactgaag gcgggtacac ctgctcctgc accgacggat attggcttct ggaaggccag 420
tgcttagaca ttgatgaatg tcgctatggg tactgccagc agctctgtgc gaatgttcct 480
ggatcctatt cttgtacatg caaccctggg tttaccctca atgaggatgg aaggtcttgc 540
caagatgtga acgagtgtgc caccgagaac ccctgcgtgc aaacctgcgt caacacctac 600
ggctctttca tctgccgctg tgacccagga tatgaacttg aggaagatgg cgttcattgc 660
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tgccaagaca tcaacgaatg tgagcacagg aaccacacgt gcaacctgca gcagacgtgc 840
tacaatttac aagggggctt caaatgcac gaccccatcc gctgtgagga gccttatctg 900
aggatcagtg ataaccgctg tatgtgtcct gctgagaacc ctggctgcag agaccagccc 960
tttaccatct tgtaccggga catggacgtg gtgtcaggac gctccgttcc cgctgacatc 1020
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gggaatgagg gcagagaatt ttacatgcgg caaacgggcc ccatcagtg caccctgggtg 1140
atgacacgcc ccatcaaagg gccccgggaa atccagctgg acttggaat gatcactgtc 1200
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taccattc 1269

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<210> 16

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

cgtttgtgca ctgctgctgt gcattcc

27

09/674379

534 Rec'd PCT/PTO 30 OCT 2000

SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> Novel polypeptides, cDNA coding these polypeptides and Use thereof

<130> ONF-2970PCT

<141> 1999-04-28

<150> JP 10-119731

<151> 1998-04-28

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<170> PatentIn Ver. 2.0

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<213> Mus musculus

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-20

-15

-10

Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp

-5

1

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Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr  
 10 15 20 25  
 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly  
 30 35 40  
 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr  
 45 50 55  
 Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala  
 60 65 70  
 Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val  
 75 80 85  
 Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val  
 90 95 100 105  
 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys  
 110 115 120  
 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp  
 125 130 135  
 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr  
 140 145 150  
 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys  
 155 160 165  
 Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val  
 170 175 180 185  
 Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr  
 190 195 200  
 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu  
 205 210 215

Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe			
220	225	230	
Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser			
235	240	245	
Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp			
250	255	260	265
Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr			
270	275	280	
Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys			
285	290	295	
Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala			
300	305	310	
Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp			
315	320	325	
Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met			
330	335	340	345
Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys			
350	355	360	
Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile			
365	370	375	
Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile			
380	385	390	
Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg			
395	400	405	
Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe			
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<211> 1344

<212> DNA

<213> Mus musculus

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ctagatattg atgaatgccg gaccatccct gaggcttgtc gtggggacat gatgtgtgtc 180  
aaccagaatg gcgggtatth gtgcatccct cgaaccaacc cagtgtatcg agggccttac 240  
tcaaatccct actctacatc ctactcaggc ccatacccag cagcggcccc accagtacca 300  
gcttccaact accccacgat ttcaaggcct cttgtctgcc gctttgggta tcagatggat 360  
gaaggcaacc agtgtgtgga tgtggacgag tgtgcaacag actcacacca gtgcaaccct 420  
accagatct gtatcaacac tgaaggaggt tacacctgct cctgcaccga tgggtactgg 480  
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gagtgtgtga accagccggg ctcatattc tgctcgtgcc ctccaggcta cgtcctgttg 840  
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gttcctgctg acatcttcca gatgcaagca acaaccgat accctggtgc ctattacatt 1140  
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atatatgtgt cgcagtatcc gttc 1344

<210> 3

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<212> DNA

<213> Mus musculus

<220>

<223> Clone mouse A55 derived from Day 13 mouse embryonic heart

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<221> CDS

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<222> (75)..(143)

<220>

<221> mat\_peptide

<222> (144)..(1418)



<400> 3

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Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile

-20

-15

ttg gca ctc tgg ctt cca cat cct ggg aat gca cag cag cag tgc aca 158

Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr

-10

-5

-1

1

5

aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat 206

Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp

10

15

20

gaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atg tgt gtc 254

Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val

25

30

35

aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat 302

Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr

40

45

50

cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac 350

Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr

55

60

65

cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca 398

Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser

70

75

80

85

agg cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag 446

Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln

90	95	100	
tgt gtg gat gtg gac gag tgt gca aca gac tca cac cag tgc aac cct	494		
Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro			
105	110	115	
acc cag atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc ac	542		
Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr			
120	125	130	
gat ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt	590		
Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys			
135	140	145	
cgc tat ggt tac tgc cag cag ctc tgt gca aat gtt cca gga tcc tat	638		
Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr			
150	155	160	165
tcc tgt aca tgc aac cct ggt ttc acc ctc aac gac gat gga agg tct	686		
Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser			
170	175	180	
tgc caa gat gtg aac gag tgc gaa act gag aat ccc tgt gtt cag acc	734		
Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr			
185	190	195	
tgt gtc aac acc tat ggc tct ttc atc tgc cgc tgt gac cca gga tat	782		
Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr			
200	205	210	
gaa ctt gag gaa gat ggc att cac tgc agt gat atg gac gag tgc agc	830		
Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser			
215	220	225	
ttc tcc gag ttc ctc tgt caa cac gag tgt gtg aac cag ccg ggc tca	878		

Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser  
230                      235                      240                      245  
tac ttc tgc tgc tgc cct cca ggc tac gtc ctg ttg gat gat aac cga 926  
Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg  
                    250                      255                      260  
agc tgc cag gat atc aat gaa tgt gag cac cga aac cac acg tgt acc 974  
Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr  
                    265                      270                      275  
tca ctg cag act tgc tac aat cta caa ggg ggc ttc aaa tgt att gat 1022  
Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp  
                    280                      285                      290  
ccc atc agc tgt gag gag cct tat ctg ctg att ggt gaa aac cgc tgt 1070  
Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys  
                    295                      300                      305  
atg tgt cct gct gag cac acc agc tgc aga gac cag cca ttc acc atc 1118  
Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile  
310                      315                      320                      325  
ctg tat cgg gac atg gat gtg gtg tca gga cgc tcc gtt cct gct gac 1166  
Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp  
                    330                      335                      340  
atc ttc cag atg caa gca aca acc cga tac cct ggt gcc tat tac att 1214  
Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile  
                    345                      350                      355  
ttc cag atc aaa tct ggc aac gag ggt cga gag ttc tat atg cgg caa 1262  
Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln  
                    360                      365                      370

aca ggg cct atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg 1310  
Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly

375

380

385

cct cgg gac atc cag ctg gac ttg gag atg atc act gtc aac act gtc 1358  
Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val

390

395

400

405

atc aac ttc aga ggc agc tcc gtg atc cga ctg cgg ata tat gtg tgc 1406  
Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser

410

415

420

cag tat ccg ttc tgagcctctg gctaaggcct ctgacactgc ctttcaccag 1458  
Gln Tyr Pro Phe

425

caccgaggga cgggaggaga aaggaaacca gcaagaatga gagcgagaca gacattgcac 1518  
ctttcctgct gaatatctcc tgggggcac agcctagcat cttgacccat atctgtacta 1578  
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ctgcgttgga agacagaggt atccagactg attaaataat tgaagaaaaa aaaaa 2233

<210> 4

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<212> PRT

<213> Mus musculus

<400> 4

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20 25 30  
Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn  
35 40 45  
Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser  
50 55 60  
Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro  
65 70 75 80  
Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu  
85 90 95  
Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln  
100 105 110  
Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys  
115 120 125  
Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile  
130 135 140  
Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro

145                      150                      155                      160  
 Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp  
                          165                      170                      175  
 Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys  
                          180                      185                      190  
 Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp  
                          195                      200                      205  
 Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp  
                          210                      215                      220  
 Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln  
 225                      230                      235                      240  
 Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp  
                          245                      250                      255  
 Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His  
                          260                      265                      270  
 Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys  
                          275                      280                      285  
 Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu  
                          290                      295                      300  
 Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro  
 305                      310                      315                      320  
 Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val  
                          325                      330                      335  
 Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala  
                          340                      345                      350  
 Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr

355                      360                      365  
 Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro  
 370                      375                      380  
 Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val  
 385                      390                      395                      400  
 Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile  
 405                      410                      415  
 Tyr Val Ser Gln Tyr Pro Phe  
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<211> 1269

<212> DNA

<213> Mus musculus

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 tatttgtgca tccctcgaac caaccagtg tatcgagggc cttactcaaa tccctactct 180  
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<210> 6

<211> 461

<212> PRT

<213> Mus musculus

<400> 6

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-35

-30

-25

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-20

-15

-10

-5

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Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro			
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Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val			
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Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe			
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Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys			
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Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr			
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Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu			
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Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln			
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Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly			
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Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys			
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Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser			
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Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile			

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His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln			
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His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro			
	240	245	250
Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu			
	255	260	265
Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn			
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Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro			
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Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr			
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Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val			
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Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr			
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Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn			
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Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr			
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Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp			
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Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser			
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420

425

&lt;210&gt; 7

&lt;211&gt; 1383

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 7

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<210> 8

<211> 2429

<212> DNA

<213> Mus musculus

<220>

<223> Clone mouse A55b derived from Day 13 mouse embryonic heart

<220>

<221> CDS

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<220>

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<222> (232).. (339)

<220>

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gactgctgac tacggcacca gcaattgctt tgctgcgacg gctgtgagac aagcagaagt 180  
ctccgaacac ttctgtctgc gtttgcctta tgtgtgtgat ttacagaggg a atg gga 237

Met Gly

-35

cct aga agt ttc gag cca atg cac agt gga ctc tgc aga cag aga cgc 285  
Pro Arg Ser Phe Glu Pro Met His Ser Gly Leu Cys Arg Gln Arg Arg

-30

-25

-20

atg ata ctc act gtt acc atc ttg gca ctc tgg ctt cca cat cct ggg 333  
Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His Pro Gly

-15

-10

-5

aat gca cag cag cag tgc aca aac ggc ttt gac ctg gac cgc cag tca 381  
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10

gga cag tgt cta gat att gat gaa tgc cgg acc atc cct gag gct tgt 429  
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15

20

25

30

cgt ggg gac atg atg tgt gtc aac cag aat ggc ggg tat ttg tgc atc 477  
Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile

35

40

45

cct cga acc aac cca gtg tat cga ggg cct tac tca aat ccc tac tct 525

Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser	
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Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala	
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Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr	
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Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr	
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Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly	
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Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys	
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160 165 170	
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Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr	
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 Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile  
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 Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu  
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 Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr  
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 Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu  
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 Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys  
 305 310 315  
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 Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser

320                      325                      330  
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 Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly  
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 Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val  
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 Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu  
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 cga ctg cgg ata tat gtg tcg cag tat ccg ttc tgagcctctg gctaaggcct 1634  
 Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe  
 415                      420                      425  
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<211> 423

<212> PRT

<213> Mus musculus

<400> 9

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 35 40 45  
 Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser  
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 65 70 75 80  
 Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu

85 90 95  
 Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln  
 100 105 110  
 Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys  
 115 120 125  
 Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile  
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 Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro  
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 Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp  
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 Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln  
 225 230 235 240  
 Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp  
 245 250 255  
 Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His  
 260 265 270  
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 275 280 285  
 Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu

290                      295                      300  
 Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro  
 305                      310                      315                      320  
 Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val  
                          325                      330                      335  
 Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala  
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 Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr  
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 Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro  
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 Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val  
 385                      390                      395                      400  
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<210> 10

<211> 1269

<212> DNA

<213> Mus musculus

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<210> 11

<211> 448

<212> PRT

<213> Homo sapiens

<400> 11

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				-5			-1	1						5	
Leu	Asp	Arg	Gln	Ser	Gly	Gln	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Arg	Thr
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Pro	Pro	Leu	Ser	Ala	Pro	Asn	Tyr	Pro	Thr	Ile	Ser	Arg	Pro	Leu	Ile
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Cys	Arg	Phe	Gly	Tyr	Gln	Met	Asp	Glu	Ser	Asn	Gln	Cys	Val	Asp	Val
90					95					100				105	
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Ile	Asn	Thr	Glu	Gly	Gly	Tyr	Thr	Cys	Ser	Cys	Thr	Asp	Gly	Tyr	Trp
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Leu	Leu	Glu	Gly	Gln	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Gly	Tyr
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Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr			
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Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu			
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Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe			
	220	225	230
Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser			
	235	240	245
Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp			
250	255	260	265
Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr			
	270	275	280
Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys			
	285	290	295
Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala			
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Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp			
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Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys			
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Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile			

365	370	375
Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile		
380	385	390
Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg		
395	400	405
Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe		
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<210> 12

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 12

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Met Pro Gly

-23

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Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys Leu Pro Ser

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 Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu  
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 His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro  
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<212> PRT

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Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp

290

295

300

Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro

305

310

315

320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val

325

330

335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala

340

345

350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr

355

360

365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro

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375

380

Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val

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